

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

09/674,377C
LFW/6
09/21/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/674,377C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 09/21/2006

PATENT APPLICATION: US/09/674,377C

TIME: 11:21:18

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw

3 <110> APPLICANT: NAKAMURA, Toshikazu
 5 <120> TITLE OF INVENTION: Neovascularization Inhibitors Derived From HGF and Methods
 6 Involving The Same (as amended)
 8 <130> FILE REFERENCE: Q61434
 10 <140> CURRENT APPLICATION NUMBER: 09/674,377C
 11 <141> CURRENT FILING DATE: 2000-10-30
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01834
 14 <151> PRIOR FILING DATE: 1999-04-06
 16 <150> PRIOR APPLICATION NUMBER: JPA 1998-134681
 17 <151> PRIOR FILING DATE: 1998-04-28
 19 <160> NUMBER OF SEQ ID NOS: 3
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 447
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: MOD_RES
 31 <222> LOCATION: (1)..(1)
 32 <223> OTHER INFORMATION: pyroglutamate
 34 <220> FEATURE:
 35 <221> NAME/KEY: CHAIN
 36 <222> LOCATION: (1)..(447)
 37 <223> OTHER INFORMATION: N-Terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)
 39 <400> SEQUENCE: 1
 41 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
 42 1 5 10 15
 45 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
 46 20 25 30
 49 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
 50 35 40 45
 53 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
 54 50 55 60
 57 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
 58 65 70 75 80
 61 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
 62 85 90 95
 65 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
 66 100 105 110
 69 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
 70 115 120 125
 73 His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
 74 130 135 140

Does Not Comply
Corrected Diskette Needed

Cp9-2,4)

RAW SEQUENCE LISTING

DATE: 09/21/2006

PATENT APPLICATION: US/09/674,377C

TIME: 11:21:18

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw

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77 Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr
78 145                      150                      155                      160
81 Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
82                      165                      170                      175
85 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
86                      180                      185                      190
89 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
90                      195                      200                      205
93 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
94                      210                      215                      220
97 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
98 225                      230                      235                      240
101 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
102                      245                      250                      255
105 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
106                      260                      265                      270
109 Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
110                      275                      280                      285
113 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
114                      290                      295                      300
117 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
118 305                      310                      315                      320
121 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
122                      325                      330                      335
125 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
126                      340                      345                      350
129 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
130                      355                      360                      365
133 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
134                      370                      375                      380
137 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
138 385                      390                      395                      400
141 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala
142                      405                      410                      415
145 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
146                      420                      425                      430
149 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
150                      435                      440                      445
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 442
155 <212> TYPE: PRT
156 <213> ORGANISM: 5 amino acid deletion
159 <220> FEATURE:
160 <221> NAME/KEY: MOD RES
161 <222> LOCATION: (1)..(1)
162 <223> OTHER INFORMATION: pyroglutamate
164 <220> FEATURE:
165 <221> NAME/KEY: CHAIN
166 <222> LOCATION: (1)..(442)

```

Invalid Response.
 12137 Responses can
 be either Artificial,
 Unknown or Genus species.
 See Item 10 on
 Error Summary
 Sheet.

RAW SEQUENCE LISTING

DATE: 09/21/2006

PATENT APPLICATION: US/09/674,377C

TIME: 11:21:19

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw

167 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF (PyrGlu32-Val478/HGF)

169 <400> SEQUENCE: 2

```

171 Glu Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
172 1          5          10          15
175 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
176          20          25          30
179 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
180          35          40          45
183 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
184          50          55          60
187 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
188 65          70          75          80
191 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
192          85          90          95
195 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
196          100         105         110
199 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
200          115         120         125
203 His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro
204          130         135         140
207 Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val
208 145          150         155         160
211 Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met
212          165         170         175
215 Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser
216          180         185         190
219 Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys
220          195         200         205
223 Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys
224          210         215         220
227 Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro
228 225          230         235         240
231 His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr
232          245         250         255
235 Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly
236          260         265         270
239 Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile
240          275         280         285
243 Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr
244          290         295         300
247 Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn
248 305          310         315         320
251 Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile
252          325         330         335
255 Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly
256          340         345         350
259 Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser
260          355         360         365
263 Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu

```

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DATE: 09/21/2006

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TIME: 11:21:19

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw

264 370 375 380
267 Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn
268 385 390 395 400
271 Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala His Gly Pro Trp Cys
272 405 410 415
275 Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg
276 420 425 430
279 Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
280 435 440
283 <210> SEQ ID NO: 3
284 <211> LENGTH: 10
285 <212> TYPE: PRT
286 <213> ORGANISM: amino acids 2-11 of human HGF alpha chain
288 <400> SEQUENCE: 3
290 Arg Lys Arg Arg Asn Thr Ile His Glu Phe
291 1 5 10

→ See Glen 10
on Error
Summary
Sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,377C

DATE: 09/21/2006

TIME: 11:21:20

Input Set : A:\Q61434.ST25.txt

Output Set: N:\CRF4\09212006\I674377C.raw